

VH CDR1	1	2	3	4	5	6	7	8	9	10 <sup>(35)</sup>
SEQ ID NO: 26 WT, 2D4	G	F	D	F	S	R	Y	W	M	S
SEQ ID NO: 43	G	F	D	F	S	<u>H</u>	Y	W	M	S
SEQ ID NO: 44	G	F	D	F	S	R	Y	W	<u>I</u>	S
SEQ ID NO: 45 DcomD7, DhuG5, DhuH8	G	F	D	F	S	R	Y	W	M	<u>T</u>
SEQ ID NO: 46 2D4H1-C3	G	F	D	F	S	R	Y	W	M	<u>A</u>
SEQ ID NO: 47	G	F	D	F	S	R	Y	W	M	<u>G</u>

Note: The sequences correspond to those shown in the sequence listing for U.S. Ser. No. 09/995,529. The column numbering reflects the residue number within each sequence listing. The small unbolded numbers above some columns indicate the numbering used to identify the positions of substitutions in the beneficial mutations described by Figure 6 of U.S. Ser. No. 09/995,529. The bolded, underlined residues are those which differ from the wild-type residue at that position.

**VH CDR1**

26: Gly Phe Asp Phe Ser Arg Tyr Trp Met Ser  
43: Gly Phe Asp Phe Ser His Tyr Trp Met Ser  
44: Gly Phe Asp Phe Ser Arg Tyr Trp Ile Ser  
45: Gly Phe Asp Phe Ser Arg Tyr Trp Met Thr  
46: Gly Phe Asp Phe Ser Arg Tyr Trp Met Ala  
47: Gly Phe Asp Phe Ser Arg Tyr Trp Met Gly

**Exhibit A**  
**US Patent Application No. 09/995,529**  
**Attorney Docket No. 30797-711.201**  
**HUIV26 CDR SUBSTITUTIONS DISCLOSED IN SPECIFICATION**

VH CDR2	1	2	3	4	5	6	7	8	9 <sup>(57)</sup>	10	11	12	13	14 <sup>(62)</sup>	15	16	17
SEQ ID NO: 28 WT, 2D4, 2D4H1- C3	E	I	N	P	D	S	S	T	I	N	Y	T	P	S	L	K	D
SEQ ID NO: 48	E	I	N	P	D	S	S	T	<u>A</u>	N	Y	T	P	S	L	K	D
SEQ ID NO: 49	E	I	N	P	D	S	S	T	<u>S</u>	N	Y	T	P	S	L	<u>D</u>	<u>K</u>
SEQ ID NO: 50	E	I	N	P	D	S	S	T	I	N	Y	T	P	<u>Y</u>	L	K	D
SEQ ID NO: 51	E	I	N	P	D	S	S	T	I	N	Y	T	P	<u>A</u>	L	K	D
SEQ ID NO: 52	E	I	N	P	D	S	S	T	I	N	Y	T	P	<u>H</u>	L	K	D
SEQ ID NO: 53	E	I	N	P	D	S	S	T	I	N	Y	T	P	<u>G</u>	L	K	D
SEQ ID NO: 54	E	I	N	P	D	S	S	T	I	N	Y	T	P	S	L	<u>Q</u>	D
SEQ ID NO: 55	E	I	N	P	D	S	S	T	I	N	Y	T	P	S	L	K	<u>S</u>
SEQ ID NO: 154	E	I	N	P	D	S	S	T	<u>A</u>	N	Y	T	P	<u>A</u>	L	K	D

**Exhibit A**  
**US Patent Application No. 09/995,529**  
**Attorney Docket No. 30797-711.201**  
**HUIV26 CDR SUBSTITUTIONS DISCLOSED IN SPECIFICATION**

VH CDR2	1	2	3	4	5	6	7	8	9 <sup>(57)</sup>	10	11	12	13	14 <sup>(62)</sup>	15	16	17
<b>SEQ ID NO: 155</b> DcomD7, DhuG5, DhuH8	E	I	N	P	D	S	S	T	<u>A</u>	N	Y	T	P	<u>Y</u>	L	K	D
<b>SEQ ID NO: 156</b>	E	I	N	P	D	S	S	T	<u>A</u>	N	Y	T	P	<u>H</u>	L	K	D
<b>SEQ ID NO: 162</b>	E	I	N	P	D	S	S	T	<u>V</u>	N	Y	T	P	S	L	K	D

Note: The sequences correspond to those shown in the sequence listing for U.S. Ser. No. 09/995,529. The column numbering reflects the residue number within each sequence listing. The small unbolded numbers above some columns indicate the numbering used to identify the positions of substitutions in the beneficial mutations described by Figure 6 of U.S. Ser. No. 09/995,529. The bolded, underlined residues are those which differ from the wild-type residue at that position.

HUIV26 CDR SUBSTITUTIONS DISCLOSED IN SPECIFICATION

VH CDR2

28: Glu Ile Asn Pro Asp Ser Ser Thr Ile Asn Tyr Thr Pro Ser Leu Lys Asp  
48: Glu Ile Asn Pro Asp Ser Ser Thr Ala Asn Tyr Thr Pro Ser Leu Lys Asp  
49: Glu Ile Asn Pro Asp Ser Ser Thr Ser Asn Tyr Thr Pro Ser Leu Asp Lys  
50: Glu Ile Asn Pro Asp Ser Ser Thr Ile Asn Tyr Thr Pro Tyr Leu Lys Asp  
51: Glu Ile Asn Pro Asp Ser Ser Thr Ile Asn Tyr Thr Pro Ala Leu Lys Asp  
52: Glu Ile Asn Pro Asp Ser Ser Thr Ile Asn Tyr Thr Pro His Leu Lys Asp  
53: Glu Ile Asn Pro Asp Ser Ser Thr Ile Asn Tyr Thr Pro Gly Leu Lys Asp  
54: Glu Ile Asn Pro Asp Ser Ser Thr Ile Asn Tyr Thr Pro Ser Leu Gln Asp  
55: Glu Ile Asn Pro Asp Ser Ser Thr Ile Asn Tyr Thr Pro Ser Leu Lys Ser  
154: Glu Ile Asn Pro Asp Ser Ser Thr Ala Asn Tyr Thr Pro Ala Leu Lys Asp  
155: Glu Ile Asn Pro Asp Ser Ser Thr Ala Asn Tyr Thr Pro Tyr Leu Lys Asp  
156: Glu Ile Asn Pro Asp Ser Ser Thr Ala Asn Tyr Thr Pro His Leu Lys Asp  
162: Glu Ile Asn Pro Asp Ser Ser Thr Val Asn Tyr Thr Pro Ser Leu Lys Asp

**Exhibit A**  
**US Patent Application No. 09/995,529**  
**Attorney Docket No. 30797-711.201**  
**HUIV26 CDR SUBSTITUTIONS DISCLOSED IN SPECIFICATION**

VH CDR3	1	2	3	4	5	6	7	8	9	10	11 (102)
SEQ ID NO: 30 WT	P	V	D	G	Y	Y	D	A	M	D	Y
SEQ ID NO: 56	P	V	<u>P</u>	G	Y	Y	D	A	M	D	Y
SEQ ID NO: 57	P	V	<u>G</u>	G	Y	Y	D	A	M	D	Y
SEQ ID NO: 58	P	V	<u>T</u>	G	Y	Y	D	A	M	D	Y
SEQ ID NO: 59	P	V	<u>A</u>	G	Y	Y	D	A	M	D	Y
SEQ ID NO: 60	P	V	D	<u>P</u>	Y	Y	D	A	M	D	Y
SEQ ID NO: 61	P	V	D	<u>A</u>	Y	Y	D	A	M	D	Y
SEQ ID NO: 62	P	V	D	<u>H</u>	Y	Y	D	A	M	D	Y
SEQ ID NO: 63 2D4, 2D4H1-C3, DcomD7, DhuG5, DhuH8	P	V	D	G	Y	Y	D	A	M	D	<u>P</u>

Exhibit A  
US Patent Application No. 09/995,529  
Attorney Docket No. 30797-711.201  
**HUIV26 CDR SUBSTITUTIONS DISCLOSED IN SPECIFICATION**

VH CDR3	1	2	3	4	5	6	7	8	9	10	11 <sup>(102)</sup>
SEQ ID NO: 64	P	V	D	G	Y	Y	D	A	M	D	<u>N</u>

Note: The sequences correspond to those shown in the sequence listing for U.S. Ser. No. 09/995,529. The column numbering reflects the residue number within each sequence listing. The small unbolded numbers above some columns indicate the numbering used to identify the positions of substitutions in the beneficial mutations described by Figure 6 of U.S. Ser. No. 09/995,529. The bolded, underlined residues are those which differ from the wild-type residue at that position.

**VH CDR3**

- 30: Pro Val Asp Gly Tyr Tyr Asp Ala Met Asp Tyr
- 56: Pro Val Pro Gly Tyr Tyr Asp Ala Met Asp Tyr
- 57: Pro Val Gly Gly Tyr Tyr Asp Ala Met Asp Tyr
- 58: Pro Val Thr Gly Tyr Tyr Asp Ala Met Asp Tyr
- 59: Pro Val Ala Gly Tyr Tyr Asp Ala Met Asp Tyr
- 60: Pro Val Asp Pro Tyr Tyr Asp Ala Met Asp Tyr
- 61: Pro Val Asp Ala Tyr Tyr Asp Ala Met Asp Tyr
- 62: Pro Val Asp His Tyr Tyr Asp Ala Met Asp Tyr
- 63: Pro Val Asp Gly Tyr Tyr Asp Ala Met Asp Pro
- 64: Pro Val Asp Gly Tyr Tyr Asp Ala Met Asp Asn

**Exhibit A**  
**US Patent Application No. 09/995,529**  
**Attorney Docket No. 30797-711.201**  
**HUIV26 CDR SUBSTITUTIONS DISCLOSED IN SPECIFICATION**

VL CDR1	1	2	3	4	5	6	7	8 <sup>(27d)</sup>	9 <sup>(27e)</sup>	10 <sup>(27f)</sup>	11	12	13	14	15	16	17
SEQ ID NO: 20 WT, 2D4, 2D4H1- C3	K	S	S	Q	S	L	L	N	S	G	N	Q	K	N	Y	L	A
SEQ ID NO: 65	K	S	S	<u>R</u>	S	L	L	N	S	G	N	Q	K	N	Y	L	A
SEQ ID NO: 66	K	S	S	<u>S</u>	S	L	L	N	S	G	N	Q	K	N	Y	L	A
SEQ ID NO: 67	K	S	S	Q	S	L	L	<u>S</u>	S	G	N	Q	K	N	Y	L	A
SEQ ID NO: 68	K	S	S	Q	S	L	L	N	<u>Y</u>	G	N	Q	K	N	Y	L	A
SEQ ID NO: 69	K	S	S	Q	S	L	L	N	<u>W</u>	G	N	Q	K	N	Y	L	A
SEQ ID NO: 70	K	S	S	Q	S	L	L	N	<u>H</u>	G	N	Q	K	N	Y	L	A
SEQ ID NO: 71	K	S	S	Q	S	L	L	N	<u>R</u>	G	N	Q	K	N	Y	L	A
SEQ ID NO: 72	K	S	S	Q	S	L	L	N	S	<u>Y</u>	N	Q	K	N	Y	L	A
SEQ ID NO: 73	K	S	S	Q	S	L	L	N	S	<u>R</u>	N	Q	K	N	Y	L	A

**Exhibit A**  
**US Patent Application No. 09/995,529**  
**Attorney Docket No. 30797-711.201**  
**HUIV26 CDR SUBSTITUTIONS DISCLOSED IN SPECIFICATION**

VL CDR1	1	2	3	4	5	6	7	8 <sup>(27d)</sup>	9 <sup>(27e)</sup>	10 <sup>(27f)</sup>	11	12	13	14	15	16	17
SEQ ID NO: 74	K	S	S	Q	S	L	L	N	S	<u>H</u>	N	Q	K	N	Y	L	A
SEQ ID NO: 75	K	S	S	Q	S	L	L	N	S	<u>I</u>	N	Q	K	N	Y	L	A
SEQ ID NO: 76	K	S	S	Q	S	L	L	N	S	G	N	<b>K</b>	K	N	Y	L	A
SEQ ID NO: 157 DcomD7, DhuG5, DhuH8	K	S	S	Q	S	L	L	N	<u>W</u>	<u>Y</u>	N	Q	K	N	Y	L	A
SEQ ID NO: 158	K	S	S	Q	S	L	L	N	<u>Y</u>	<u>Y</u>	N	Q	K	N	Y	L	A
SEQ ID NO: 159	K	S	S	Q	S	L	L	N	<u>Y</u>	<u>H</u>	N	Q	K	N	Y	L	A
SEQ ID NO: 160	K	S	S	Q	S	L	L	N	<u>R</u>	<u>Y</u>	N	Q	K	N	Y	L	A
SEQ ID NO: 161	K	S	S	Q	S	L	L	N	<u>W</u>	<u>H</u>	N	Q	K	N	Y	L	A

Note: The sequences correspond to those shown in the sequence listing for U.S. Ser. No. 09/995,529. The column numbering reflects the residue number within each sequence listing. The small unbolded numbers above some columns indicate the numbering used to identify the positions of substitutions in the beneficial mutations described by Figure 6 of U.S. Ser. No. 09/995,529. The bolded, underlined residues are those which differ from the wild-type residue at that position.



**HUIV26 CDR SUBSTITUTIONS DISCLOSED IN SPECIFICATION**

VL CDR1	20:	Lys	Ser	Ser	Gln	Ser	Leu	Leu	Asn	Ser	Gly	Asn	Gln	Lys	Asn	Tyr	Leu	Ala
	65:	Lys	Ser	Ser	Arg	Ser	Leu	Leu	Asn	Ser	Gly	Asn	Gln	Lys	Asn	Tyr	Leu	Ala
	66:	Lys	Ser	Ser	Ser	Ser	Leu	Leu	Asn	Ser	Gly	Asn	Gln	Lys	Asn	Tyr	Leu	Ala
	67:	Lys	Ser	Ser	Gln	Ser	Leu	Leu	Ser	Ser	Gly	Asn	Gln	Lys	Asn	Tyr	Leu	Ala
	68:	Lys	Ser	Ser	Gln	Ser	Leu	Leu	Asn	Tyr	Gly	Asn	Gln	Lys	Asn	Tyr	Leu	Ala
	69:	Lys	Ser	Ser	Gln	Ser	Leu	Leu	Asn	Trp	Gly	Asn	Gln	Lys	Asn	Tyr	Leu	Ala
	70:	Lys	Ser	Ser	Gln	Ser	Leu	Leu	Asn	His	Gly	Asn	Gln	Lys	Asn	Tyr	Leu	Ala
	71:	Lys	Ser	Ser	Gln	Ser	Leu	Leu	Asn	Arg	Gly	Asn	Gln	Lys	Asn	Tyr	Leu	Ala
	72:	Lys	Ser	Ser	Gln	Ser	Leu	Leu	Asn	Ser	Tyr	Asn	Gln	Lys	Asn	Tyr	Leu	Ala
	73:	Lys	Ser	Ser	Gln	Ser	Leu	Leu	Asn	Ser	Arg	Asn	Gln	Lys	Asn	Tyr	Leu	Ala
	74:	Lys	Ser	Ser	Gln	Ser	Leu	Leu	Asn	Ser	His	Asn	Gln	Lys	Asn	Tyr	Leu	Ala
	75:	Lys	Ser	Ser	Gln	Ser	Leu	Leu	Asn	Ser	Ile	Asn	Gln	Lys	Asn	Tyr	Leu	Ala
	76:	Lys	Ser	Ser	Gln	Ser	Leu	Leu	Asn	Ser	Gly	Asn	Lys	Lys	Asn	Tyr	Leu	Ala
	157:	Lys	Ser	Ser	Gln	Ser	Leu	Leu	Asn	Trp	Tyr	Asn	Gln	Lys	Asn	Tyr	Leu	Ala
	158:	Lys	Ser	Ser	Gln	Ser	Leu	Leu	Asn	Tyr	Tyr	Asn	Gln	Lys	Asn	Tyr	Leu	Ala
	159:	Lys	Ser	Ser	Gln	Ser	Leu	Leu	Asn	Tyr	His	Asn	Gln	Lys	Asn	Tyr	Leu	Ala
	160:	Lys	Ser	Ser	Gln	Ser	Leu	Leu	Asn	Arg	Tyr	Asn	Gln	Lys	Asn	Tyr	Leu	Ala
	161:	Lys	Ser	Ser	Gln	Ser	Leu	Leu	Asn	Trp	His	Asn	Gln	Lys	Asn	Tyr	Leu	Ala

VL CDR2	1	2	3	4	5	6	7
SEQ ID NO: 22 WT, 2D4, 2D4H1- C3, DcomD7, DhuG5, DhuH8	G	A	S	T	R	E	S

Note: The sequences correspond to those shown in the sequence listing for U.S. Ser. No. 09/995,529. The column numbering reflects the residue number within each sequence listing.

VL CDR2

22: Gly Ala Ser Thr Arg Glu Ser

VL CDR3	1	2	3	4	5 <sup>(93)</sup>	6	7	8	9
SEQ ID NO: 24 WT	Q	N	D	H	S	Y	P	Y	T
SEQ ID NO: 77 2D4, 2D4H1-C3, DcomD7, DhuG5, DhuH8	Q	N	D	H	<b><u>Q</u></b>	Y	P	Y	T
SEQ ID NO: 78	Q	N	D	H	<b><u>G</u></b>	Y	P	Y	T
SEQ ID NO: 79	Q	N	D	H	<b><u>L</u></b>	Y	P	Y	T
SEQ ID NO: 80	Q	N	D	H	<b><u>A</u></b>	Y	P	Y	T
SEQ ID NO: 81	Q	N	D	H	<b><u>T</u></b>	Y	P	Y	T
SEQ ID NO: 82	Q	N	D	H	<b><u>V</u></b>	Y	P	Y	T
SEQ ID NO: 83	Q	N	D	H	S	<b><u>N</u></b>	P	Y	T
SEQ ID NO: 84	Q	N	D	H	S	<b><u>S</u></b>	P	Y	T
SEQ ID NO: 85	Q	N	D	H	S	<b><u>P</u></b>	P	Y	T
SEQ ID NO: 86	Q	N	D	H	S	<b><u>M</u></b>	P	Y	T

Note: The sequences correspond to those shown in the sequence listing for U.S. Ser. No. 09/995,529. The column numbering reflects the residue number within each sequence listing. The small unbolded numbers above some columns indicate the numbering used to identify the positions of substitutions in the beneficial mutations described by Figure 6 of U.S. Ser. No. 09/995,529. The bolded, underlined residues are those which differ from the wild-type residue at that position.

**VL CDR3**

24: Gln Asn Asp His Ser Tyr Pro Tyr Thr  
77: Gln Asn Asp His Gln Tyr Pro Tyr Thr  
78: Gln Asn Asp His Gly Tyr Pro Tyr Thr  
79: Gln Asn Asp His Leu Tyr Pro Tyr Thr  
80: Gln Asn Asp His Ala Tyr Pro Tyr Thr  
81: Gln Asn Asp His Thr Tyr Pro Tyr Thr  
82: Gln Asn Asp His Val Tyr Pro Tyr Thr  
83: Gln Asn Asp His Ser Asn Pro Tyr Thr  
84: Gln Asn Asp His Ser Ser Pro Tyr Thr  
85: Gln Asn Asp His Ser Pro Pro Tyr Thr  
86: Gln Asn Asp His Ser Met Pro Tyr Thr